

SEQUENCE LISTING

<110> Klucher, Kevin M.
Sivakumar, Pallavur V.
Kindsvogel, Wayne R.
Henderson, Katherine E.

<120> METHODS FOR TREATING VIRAL INFECTION
USING IL-28 AND IL-29

<130> 02-24

<150> US 60/420,714
<151> 2002-10-23

<150> US 60/463,939
<151> 2003-04-18

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acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct ctc ccg 96
Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala Leu Pro
20 25 30

gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
50 55 60

ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg	240
Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp	
65 70 75 80	
gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg gag gct	288
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala	
85 90 95	
gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac	336
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp	
100 105 110	
cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg cac cat	384
Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His	
115 120 125	
atc ctc tcc cag ttc cgg gcc tgt gtg agt cgt cag ggc ctg ggc acc	432
Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr	
130 135 140	
cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc	480
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu	
145 150 155 160	
cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag tcc cct	528
His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro	
165 170 175	
ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc ctc acg	576
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
180 185 190	
cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga	618
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *	
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 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60
 Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala
 85 90 95
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110
 Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125
 Ile Leu Ser Gln Phe Arg Ala Cys Val Ser Arg Gln Gly Leu Gly Thr

130	135	140	
Gln Ile Gln Pro Gln Pro	Thr Ala Gly Pro	Arg Thr Arg Gly Arg	
145	150	155	160
His His Trp Leu Tyr Arg	Leu Gln Glu Ala	Pro Lys Lys Glu Ser	Pro
	165	170	175
Gly Cys Leu Glu Ala Ser	Val Thr Phe Asn	Leu Phe Arg	Leu Leu Thr
	180	185	190
Arg Asp Leu Asn Cys Val	Ala Ser Gly Asp	Leu Cys Val	
	195	200	205

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1 5 10 15

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gcc gtg gca ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag  96
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
                     20          25          30

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ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg 144
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
          35           40           45

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  agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa 192
  Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
      50          55          60

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aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg 240
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
 65          70          75          80

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ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc 288
 Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
 85 90 95

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ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac 336
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
          100          105          110

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gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc 384
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
 115 120 125

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cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc 432
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
130          135          140

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cgc ctc cac cac tgg ctg cac cg^g ctc cag gag gcc ccc aaa aag gag 480

Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu			
145	150	155	160
tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc			528
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
165	170	175	
ctc acg cga gac ctc aaa tat gtg gcc gat ggg gac ctg tgt ctg aga			576
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg			
180	185	190	
acg tca acc cac cct gag tcc acc tga			603
Thr Ser Thr His Pro Glu Ser Thr *			
195	200		

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20	25	30	
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala			
35	40	45	
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys			
50	55	60	
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg			
65	70	75	80
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala			
85	90	95	
Leu Thr Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp			
100	105	110	
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu			
115	120	125	
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly			
130	135	140	
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu			
145	150	155	160
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu			
165	170	175	
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg			
180	185	190	
Thr Ser Thr His Pro Glu Ser Thr			
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acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg 96
 Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro
 20 25 30

gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct cca cag 144
 Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln
 35 40 45

gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt 192
 Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu
 50 55 60

ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg 240
 Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp
 65 70 75 80

gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct 288
 Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala
 85 90 95

gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac act gac 336
 Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp
 100 105 110

cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg cac cat 384
 Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His
 115 120 125

atc ctc tcc cag ctc cgg gcc tgt gtg agt cgt cag ggc ccg ggc acc 432
 Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr
 130 135 140

cag atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc cgc ctc 480
 Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu
 145 150 155 160

cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag tcc cct 528
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro
 165 170 175

ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc acg 576
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 180 185 190

cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc 615
 Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 195 200 205

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Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln			
35	40	45	
Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu			
50	55	60	
Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp			
65	70	75	80
Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala			
85	90	95	
Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp			
100	105	110	
Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu His His			
115	120	125	
Ile Leu Ser Gln Leu Arg Ala Cys Val Ser Arg Gln Gly Pro Gly Thr			
130	135	140	
Gln Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu			
145	150	155	160
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro			
165	170	175	
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr			
180	185	190	
Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val			
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			1			5					10		

ctc	ctc	ctg	ttg	cct	ctg	ctg	gcc	gca	gtg	ctg	aca	aga	acc	99
Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Ala	Val	Leu	Thr	Arg	Thr	
15						20					25			

caa	gct	gac	cct	gtc	ccc	agg	gcc	acc	agg	ctc	cca	gtg	gaa	gca	aag	147
Gln	Ala	Asp	Pro	Val	Pro	Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	
30						35					40					

gat	tgc	cac	att	gct	cag	ttc	aag	tct	ctg	tcc	cca	aaa	gag	ctg	cag	195
Asp	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	
45						50					55					

gcc	ttc	aaa	aag	gcc	aag	gat	gcc	atc	gag	aag	agg	ctg	ctt	gag	aag	243
Ala	Phe	Lys	Ala	Lys	Asp	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys		
60					65				70							

gac	ctg	agg	tgc	agt	tcc	cac	ctc	ttc	ccc	agg	gcc	tgg	gac	ctg	aag	291
Asp	Leu	Arg	Cys	Ser	Ser	His	Leu	Phe	Pro	Arg	Ala	Trp	Asp	Leu	Lys	
75						80			85		90					

cag	ctg	cag	gtc	caa	gag	cgc	ccc	aag	gcc	ttg	cag	gct	gag	gtg	gcc	339
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Gln	Leu	Gln	Val	Gln	Glu	Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala	
95										100					105	
ctg	acc	ctg	aag	gtc	tgg	gag	aac	atg	act	gac	tca	gcc	ctg	gcc	acc	387
Leu	Thr	Leu	Lys	Val	Trp	Glu	Asn	Met	Thr	Asp	Ser	Ala	Leu	Ala	Thr	
110									115					120		
atc	ctg	ggc	cag	cct	ctt	cat	aca	ctg	agc	cac	att	cac	tcc	cag	ctg	435
Ile	Leu	Gly	Gln	Pro	Leu	His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu	
125									130				135			
cag	acc	tgt	aca	cag	ctt	cag	gcc	aca	gca	gag	ccc	agg	tcc	ccg	agc	483
Gln	Thr	Cys	Thr	Gln	Leu	Gln	Ala	Thr	Ala	Glu	Pro	Arg	Ser	Pro	Ser	
140									145				150			
cgc	cgc	ctc	tcc	cgc	tgg	ctg	cac	agg	ctc	cag	gag	gcc	cag	agc	aag	531
Arg	Arg	Leu	Ser	Arg	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys	
155									160				165			170
gag	acc	cct	ggc	tgc	ctg	gag	gcc	tct	gtc	acc	tcc	aac	ctg	ttt	cgc	579
Glu	Thr	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Ser	Asn	Leu	Phe	Arg	
175									180					185		
ctg	ctc	acc	cgg	gac	ctc	aag	tgt	gtg	gcc	aat	gga	gac	cag	tgt	gtc	627
Leu	Leu	Thr	Arg	Asp	Leu	Lys	Cys	Val	Ala	Asn	Gly	Asp	Gln	Cys	Val	
190									195					200		
tga	cct															633
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									20				25		30	
Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	Asp	Cys	His	Ile	Ala	Gln	
									35				40		45	
Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	Ala	Phe	Lys	Lys	Ala	Lys	
									50				55		60	
Asp	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys	Asp	Leu	Arg	Cys	Ser	Ser	
									65				70		75	80
His	Leu	Phe	Pro	Arg	Ala	Trp	Asp	Leu	Lys	Gln	Leu	Gln	Val	Gln	Glu	
									85				90		95	
Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala	Leu	Thr	Leu	Lys	Val	Trp	
									100				105		110	
Glu	Asn	Met	Thr	Asp	Ser	Ala	Leu	Ala	Thr	Ile	Leu	Gly	Gln	Pro	Leu	
									115				120		125	
His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu	Gln	Thr	Cys	Thr	Gln	Leu	
									130				135		140	
Gln	Ala	Thr	Ala	Glu	Pro	Arg	Ser	Pro	Ser	Arg	Arg	Leu	Ser	Arg	Trp	
									145				150		155	160
Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys	Glu	Thr	Pro	Gly	Cys	Leu	
									165				170		175	
Glu	Ala	Ser	Val	Thr	Ser	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg	Asp	Leu	
									180				185		190	

Lys Cys Val Ala Asn Gly Asp Gln Cys Val
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				1					5				10			
ctc	ctc	ctg	ctg	ttg	cct	ctg	ctg	gcc	gca	gtg	ctg	aca	aga	acc	99	
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Ala	Ala	Val	Leu	Thr	Arg	Thr	
				15				20				25				
caa	gct	gac	cct	gtc	ccc	agg	gcc	acc	agg	ctc	cca	gtg	gaa	gca	aag	147
Gln	Ala	Asp	Pro	Val	Pro	Arg	Ala	Thr	Arg	Leu	Pro	Val	Glu	Ala	Lys	
				30			35					40				
gat	tgc	cac	att	gct	cag	ttc	aag	tct	ctg	tcc	cca	aaa	gag	ctg	cag	195
Asp	Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Lys	Glu	Leu	Gln	
				45			50					55				
gcc	ttc	aaa	aag	gcc	aag	ggt	gcc	atc	gag	aag	agg	ctg	ctt	gag	aag	243
Ala	Phe	Lys	Lys	Ala	Lys	Gly	Ala	Ile	Glu	Lys	Arg	Leu	Leu	Glu	Lys	
				60			65					70				
gac	atg	agg	tgc	agt	tcc	cac	ctc	atc	tcc	agg	gcc	tgg	gac	ctg	aag	291
Asp	Met	Arg	Cys	Ser	Ser	His	Leu	Ile	Ser	Arg	Ala	Trp	Asp	Leu	Lys	
				75			80					85			90	
cag	ctg	cag	gtc	caa	gag	cgc	ccc	aag	gcc	ttg	cag	gct	gag	gtg	gcc	339
Gln	Leu	Gln	Val	Gln	Glu	Arg	Pro	Lys	Ala	Leu	Gln	Ala	Glu	Val	Ala	
				95				100					105			
ctg	acc	ctg	aag	gtc	tgg	gag	aac	ata	aat	gac	tca	gcc	ctg	acc	acc	387
Leu	Thr	Leu	Lys	Val	Trp	Glu	Asn	Ile	Asn	Asp	Ser	Ala	Leu	Thr	Thr	
				110			115					120				
atc	ctg	ggc	cag	cct	ctt	cat	aca	ctg	agc	cac	att	cac	tcc	cag	ctg	435
Ile	Leu	Gly	Gln	Pro	Leu	His	Thr	Leu	Ser	His	Ile	His	Ser	Gln	Leu	
				125			130					135				
cag	acc	tgt	aca	cag	ctt	cag	gcc	aca	gca	gag	ccc	aag	ccc	ccg	agt	483
Gln	Thr	Cys	Thr	Gln	Leu	Gln	Ala	Thr	Ala	Glu	Pro	Lys	Pro	Pro	Ser	
				140			145					150				
cgc	cgc	ctc	tcc	cgc	tgg	ctg	cac	agg	ctc	cag	gag	gcc	cag	agc	aag	531
Arg	Arg	Leu	Ser	Arg	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Gln	Ser	Lys	
				155			160					165			170	
gag	act	cct	ggc	tgc	ctg	gag	gac	tct	gtc	acc	tcc	aac	ctg	ttt	caa	579
Glu	Thr	Pro	Gly	Cys	Leu	Glu	Asp	Ser	Val	Thr	Ser	Asn	Leu	Phe	Gln	
				175			180					185				

ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc	627		
Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val			
190	195	195	200
195	200		

tga cc	632
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<210> 10
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Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro	
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Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln	
35 40 45	
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys	
50 55 60	
Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser	
65 70 75 80	
His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu	
85 90 95	
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp	
100 105 110	
Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu	
115 120 125	
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu	
130 135 140	
Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp	
145 150 155 160	
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu	
165 170 175	
Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu	
180 185 190	
Lys Cys Val Ala Ser Gly Asp Gln Cys Val	
195 200	

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<220>
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<221> misc_feature
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Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln	
1 5 10 15	

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	96
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Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu			
20	25	30	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc			144
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly			
35	40	45	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc			192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr			
50	55	60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgg gca acc aag gag ctg			240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu			
65	70	75	80
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc			288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe			
85	90	95	
aag gga cgc gtc cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg			336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val			
100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag cgg gcc cca cct			384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro			
115	120	125	
gtc ctg gtc acc cag acg gag atc ctg agt gcc aat gcc acg			432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
130	135	140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtc			480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val			
145	150	155	160
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act			528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr			
165	170	175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa			576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu			
180	185	190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa			624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys			
195	200	205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa			672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu			
210	215	220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta			720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu			
225	230	235	240
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc			768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro			
245	250	255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gac ttt tct gga cac			816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His			
260	265	270	

aca cac cct gtg gca acc ttt cag ccc agc aga cca gag tcc gtg aat	864
Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn	
275 280 285	
gac ttg ttc ctc tgt ccc caa aag gaa ctg acc aga ggg gtc agg ccg	912
Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro	
290 295 300	
acg cct cga gtc agg gcc cca gcc acc caa cag aca aga tgg aag aag	960
Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys	
305 310 315 320	
gac ctt gca gag gac gaa gag gag gat gag gag gac aca gaa gat	1008
Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp	
325 330 335	
ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc ctg ggg caa	1056
Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln	
340 345 350	
gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg gac tca ggg	1104
Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly	
355 360 365	
agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct gct tgg gat	1152
Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp	
370 375 380	
tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc tgg gac agg	1200
Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg	
385 390 395 400	
gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg	1248
Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro	
405 410 415	
ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag	1296
Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Glu Phe Ser Lys	
420 425 430	
gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg	1344
Asp Ser Gly Phe Leu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp	
435 440 445	
gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga	1392
Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly	
450 455 460	
ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct	1440
Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro	
465 470 475 480	
gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg	1488
Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala	
485 490 495	
ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg	1536
Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg	
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aca ttg ggg cat tac atg gcc agg tga	1563

Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 12
 <211> 520
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365
 Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415

Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
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 Thr Leu Gly His Tyr Met Ala Arg
 515 520

<210> 13
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1476)

<221> misc_feature
 <222> (0)...(0)
 <223> IL-28RA splice variant

<400> 13

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Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln	
1		5						10					15			

gcc	gct	cca	ggg	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	96
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
20					25							30				

ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
35					40							45				

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
50					55						60					

cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
65					70				75			80				

cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
85					90							95				

aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
100					105						110					

gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
115					120						125					

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	528
Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctc cca tcg ctt ctg ata ctg ctg tta	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu	
225 230 235 240	
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro	
245 250 255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly	
260 265 270	
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg	
275 280 285	
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp	
290 295 300	
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe	
305 310 315 320	
ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg	1008
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val	
325 330 335	
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser	
340 345 350	
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc	1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser	
355 360 365	
tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc	1152
Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly	

370	375	380	
caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa			1200
Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu			
385 390 395 400			
ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc			1248
Phe Ser Lys Asp Ser Gly Phe Leu Glu Leu Pro Glu Asp Asn Leu			
405 410 415			
tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc			1296
Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val			
420 425 430			
cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa			1344
Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu			
435 440 445			
agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac			1392
Ser Ser Pro Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp			
450 455 460			
agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac			1440
Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp			
465 470 475 480			
agg ggc cgg aca ttg ggg cat tac atg gcc agg tga			1476
Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg *			
485 490			

<210> 14
 <211> 491
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
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 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys

195	200	205
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu	Glu Val Pro Glu	
210 215 220		
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu		
225 230 235 240		
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro		
245 250 255		
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly		
260 265 270		
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg		
275 280 285		
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Asp Glu Glu Asp		
290 295 300		
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe		
305 310 315 320		
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val		
325 330 335		
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser		
340 345 350		
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser		
355 360 365		
Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly		
370 375 380		
Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu		
385 390 395 400		
Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu		
405 410 415		
Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val		
420 425 430		
Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu		
435 440 445		
Ser Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp		
450 455 460		
Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp		
465 470 475 480		
Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg		
485 490		

<210> 15
<211> 674
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)...(636)

<221> misc_feature
<222> (0)...(0)
<223> IL-28RA soluble variant

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1 5 10 15		
gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg		96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu		
20 25 30		
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc		144

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly			
35	40	45	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc			192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr			
50	55	60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg			240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu			
65	70	75	80
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc			288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe			
85	90	95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg			336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val			
100	105	110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct			384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro			
115	120	125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg			432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr			
130	135	140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg			480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val			
145	150	155	160
gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct			528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro			
165	170	175	
gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc			576
Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe			
180	185	190	
tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct			624
Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro			
195	200	205	
gta cac tcc tga cttctggcag tcagccctaa taaaatctga tcaaagta			674
Val His Ser *			
210			

<210> 16
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 16
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 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60

Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205
 Val His Ser
 210

<210> 17

<211> 734

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> (53)....(127)

<221> mat_peptide

<222> (128)....(655)

<221> CDS

<222> (53)....(655)

<400> 17

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 Met Lys
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 Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala
 -20 -15 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct 154
 Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala
 -5 1 5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct 202
 Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10 15 20 25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag 250
 Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
 30 35 40

tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg 298
 Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg
 45 50 55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg	346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu	
60 65 70	
gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac	394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp	
75 80 85	
act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg	442
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Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val	
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 Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
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 85 90 95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct 499
 His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
 100 105 110 115

cag ccc aca gca ggg ccc agg ccc cg ^g ggc cgc ctc cac cac tgg ctg	547																																																																																																																							
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu																																																																																																																								
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Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu
60                      65                      70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac 394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
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90                      95                      100                     105

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His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr
110                     115                     120

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Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val			
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Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr			
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Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His			
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Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln			
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Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His			
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Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser	
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Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr	
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Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe	
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Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu	
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tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc	480
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 35 40 45
 Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu

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Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp				
	85	90	95	
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe				
	100	105	110	
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Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu				
	130	135	140	
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu				
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Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
	165	170	175	

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<210> 25
<211> 531
<212> DNA
<213> Artificial Sequence
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<220>
<223> met IL-28A mutant C49S

<221> CDS
<222> (1) ... (531)

<400> 25
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

tcc	agg	tgc	cac	tcc	cgc	ctc	ttc	ccc	agg	acc	tgg	gac	ctg	agg	cag	192
Ser	Arg	Cys	His	Ser	Arg	Leu	Phe	Pro	Arg	Thr	Trp	Asp	Leu	Arg	Gln	
50				55						60						

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

```

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg  288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85          90          95

```

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gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
          100          105          110

```

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aaq 432

Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys				
130	135	140		
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc				480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg				
145	150	155	160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc				528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
165	170	175		
tga				531
*				

<210> 26
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C49S

<400> 26				
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly				
1	5	10	15	
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala				
20	25	30		
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp				
35	40	45		
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln				
50	55	60		
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu				
65	70	75	80	
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val				
85	90	95		
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln				
100	105	110		
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg				
115	120	125		
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys				
130	135	140		
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg				
145	150	155	160	
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val				
165	170	175		

<210> 27
 <211> 528
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C50S

<221> CDS
 <222> (1)...(528)

<400> 27
 gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48

Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys				
1 5 10 15				
cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt				96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe				
20 25 30				
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc				144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys				
35 40 45				
agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg				192
Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu				
50 55 60				
cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg				240
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr				
65 70 75 80				
ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac				288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp				
85 90 95				
gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc				336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe				
100 105 110				
cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc				384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly				
115 120 125				
cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag				432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu				
130 135 140				
tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc				480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu				
145 150 155 160				
ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga				528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *				
165 170 175				

<210> 28
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-28A mutant C50S

<400> 28
 Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1 5 10 15
 His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
 20 25 30
 Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp Cys
 35 40 45

Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
 85 90 95
 Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
 100 105 110
 Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
 115 120 125
 Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
 130 135 140
 Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
 145 150 155 160
 Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 29
 <211> 531
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-28A mutant C51S

<221> CDS
 <222> (1)...(531)

<400> 29
 atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
 Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg 288
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

ggc cgc ctc cac cat tgg ctg tac cg ^g ctc cag gag gcc cca aaa aag	432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc	480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc	528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	
tga	531
*	

<210> 30
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C51S

<400> 30	
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly	
1 5 10 15	
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp	
35 40 45	
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu	
65 70 75 80	
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val	
85 90 95	
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln	
100 105 110	
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg	
115 120 125	
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys	
130 135 140	
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg	
145 150 155 160	
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val	
165 170 175	

<210> 31
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<221> CDS
<222> (1)...(546)

<400> 31

ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac	48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His	
1 5 10 15	
atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa	96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys	
20 25 30	
aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct	144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser	
35 40 45	
tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag	192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln	
50 55 60	
gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg	240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu	
65 70 75 80	
aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat	288
Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp	
85 90 95	
cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc	336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys	
100 105 110	
att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac	384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His	
115 120 125	
cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt	432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly	
130 135 140	
tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt	480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg	
145 150 155 160	
gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc	528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr	
165 170 175	
cat ccg gaa tct acc taa	546
His Pro Glu Ser Thr *	
180	

<210> 32
 <211> 181
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-29 mutant C171S

<400> 32
 Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys His
 1 5 10 15
 Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
 20 25 30

Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp	Ser
35					40					45					
Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu	Gln
50					55					60					
Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	Thr	Leu
65					70					75					80
Lys	Val	Leu	Glu	Ala	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	Asp
	85					90					95				
Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala	Cys
	100					105					110				
Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Pro	Arg	Gly	Arg	Leu	His
	115					120					125				
His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	Glu	Ser	Ala	Gly
	130					135					140				
Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	Leu	Leu	Thr	Arg
	145					150					155				160
Asp	Leu	Lys	Tyr	Val	Ala	Asp	Gly	Asn	Leu	Ser	Leu	Arg	Thr	Ser	Thr
					165					170					175
His	Pro	Glu	Ser	Thr											
					180										

<210> 33
 <211> 549
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-29 mutant C172S

<221> CDS
 <222> (1)...(549)

<400> 33															
atg	ggt	ccg	gtt	ccg	acc	tct	aaa	cca	acc	acc	act	ggt	aaa	ggt	tgc
Met	Gly	Pro	Val	Pro	Thr	Ser	Lys	Pro	Thr	Thr	Thr	Gly	Lys	Gly	Cys
1					5				10				15		
cac	atc	ggt	cgt	ttc	aaa	tct	ctg	tct	ccg	cag	gaa	ctg	gct	tct	ttc
His	Ile	Gly	Arg	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Ala	Ser	Phe
					20				25			30			
aaa	aaa	gct	cgt	gac	gct	ctg	gaa	gaa	tct	ctg	aaa	ctg	aaa	aac	tgg
Lys	Lys	Ala	Arg	Asp	Ala	Leu	Glu	Glu	Ser	Leu	Lys	Leu	Lys	Asn	Trp
					35				40			45			
tct	tgc	tct	tct	ccg	gtt	ttc	ccg	ggt	aac	tgg	gat	ctg	cgt	ctg	ctg
Ser	Cys	Ser	Ser	Pro	Val	Phe	Pro	Gly	Asn	Trp	Asp	Leu	Arg	Leu	Leu
					50				55			60			
cag	gtt	cgt	gaa	cgt	ccg	gtt	ctg	gaa	gct	gaa	ctg	gct	ctg	acc	
Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Leu	Ala	Glu	Leu	Ala	Thr
					65				70			75			80
ctg	aaa	gtt	ctg	gaa	gct	gca	ggt	cct	gct	ctg	gaa	gat	gtt	ctg	
Leu	Lys	Val	Leu	Glu	Ala	Ala	Gly	Pro	Ala	Leu	Glu	Asp	Val	Leu	
					85				90			95			
gat	cag	ccg	ctg	cac	act	ctg	cac	cac	atc	ctg	tct	cag	ctg	cag	gct
Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	Leu	Gln	Ala
					100				105			110			

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	
cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	
ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc	480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145 150 155 160	
cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct	528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser	
165 170 175	
acc cat ccg gaa tct acc taa	549
Thr His Pro Glu Ser Thr *	
180	

<210> 34
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-29 mutant C172S

<400> 34
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
 1 5 10 15
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45
 Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
 50 55 60
 Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65 70 75 80
 Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
 85 90 95
 Asp Gln Pro Leu His Thr Leu His Ile Leu Ser Gln Leu Gln Ala
 100 105 110
 Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
 145 150 155 160

Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

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<210> 35
<211> 531
<212> DNA
<213> Artificial Sequence
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<220>
<223> met IL-28A

<221> CDS
<222> (1) . . . (531)

<400> 35
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc	96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala	
20 25 30	

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45

tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag	192
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln	
50 55 60	

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg 240
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80

```

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg  288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85          90          95

```

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gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
          100          105          110

```

ttc cg^g gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cg^g 384
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125

```

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag 432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130          135          140

```

```

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc 480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145           150           155           160

```

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc 528
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

tga
*

531

<210> 36
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> met IL-28A

<400> 36
 Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1 5 10 15
 Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
 20 25 30
 Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
 35 40 45
 Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
 50 55 60
 Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65 70 75 80
 Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
 85 90 95
 Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
 100 105 110
 Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
 115 120 125
 Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
 130 135 140
 Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
 145 150 155 160
 Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
 165 170 175

<210> 37
 <211> 621
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> met IL-29

<221> CDS
 <222> (1)...(549)

<400> 37
 atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc 48
 Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Gly Lys Gly Cys
 1 5 10 15
 cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc 96
 His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
 20 25 30
 aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg 144
 Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
 35 40 45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc	192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	
cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg	240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta	288
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	
gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc	336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	
tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc	384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu	
115 120 125	
cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct	432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala	
130 135 140	
ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg	480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr	
145 150 155 160	
cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca	528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser	
165 170 175	
acc cac cct gag tcc acc tga caccccacac cttattttatg cgctgagccc	579
Thr His Pro Glu Ser Thr *	
180	
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35 40 45	
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu	
50 55 60	
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr	
65 70 75 80	
Leu Lys Val Leu Glu Ala Ala Gly Pro Ala Leu Glu Asp Val Leu	
85 90 95	
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala	
100 105 110	

Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
 115 120 125
 His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
 130 135 140
 Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
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 Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
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 Thr His Pro Glu Ser Thr
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Met	Val	Pro	Val	Ala	Arg	Leu	Arg	Gly	Ala	Leu	Pro	Asp	Ala	Arg	Gly	
1		5				10					15					

tgc	cac	ata	gcc	cag	ttc	aag	tcc	ctg	tct	cca	cag	gag	ctg	cag	gcc	96
Cys	His	Ile	Ala	Gln	Phe	Lys	Ser	Leu	Ser	Pro	Gln	Glu	Leu	Gln	Ala	
20			25					30								

ttt	aag	agg	gcc	aaa	gat	gcc	tta	gaa	gag	tcg	ctt	ctg	ctg	aag	gac	144
Phe	Lys	Arg	Ala	Lys	Asp	Ala	Leu	Glu	Ser	Leu	Leu	Leu	Lys	Asp		
35			40				45									

tgc	aag	tgc	cgc	tcc	cgc	ctc	ttc	ccc	agg	acc	tgg	gac	ctg	agg	cag	192
Cys	Lys	Cys	Arg	Ser	Arg	Leu	Phe	Pro	Arg	Thr	Trp	Asp	Leu	Arg	Gln	
50			55			60										

ctg	cag	gtg	agg	gag	cgc	ccc	gtg	gct	ttg	gag	gct	gag	ctg	gcc	ctg	240
Leu	Gln	Val	Arg	Glu	Arg	Pro	Val	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Leu	
65			70			75			80							

acg	ctg	aag	gtt	ctg	gag	gcc	acc	gct	gac	act	gac	cca	gcc	ctg	ggg	288
Thr	Leu	Lys	Val	Leu	Glu	Ala	Thr	Ala	Asp	Thr	Asp	Pro	Ala	Leu	Gly	
85			90			95										

gat	gtc	ttg	gac	cag	ccc	ctt	cac	acc	ctg	cac	cat	atc	ctc	tcc	cag	336
Asp	Val	Leu	Asp	Gln	Pro	Leu	His	Thr	Leu	His	His	Ile	Leu	Ser	Gln	
100			105			110										

ctc	cgg	gcc	tgt	atc	cag	cct	cag	ccc	acg	gca	ggg	ccc	agg	acc	cgg	384
Leu	Arg	Ala	Cys	Ile	Gln	Pro	Gln	Pro	Thr	Ala	Gly	Pro	Arg	Thr	Arg	
115			120			125										

ggc	cgc	ctc	cac	cat	tgg	ctg	cac	cgg	ctc	cag	gag	gcc	cca	aaa	aag	432
Gly	Arg	Leu	His	His	Trp	Leu	His	Arg	Leu	Gln	Glu	Ala	Pro	Lys	Lys	
130			135			140										

gag	tcc	cct	ggc	tgc	ctc	gag	gcc	tct	gtc	acc	ttc	aac	ctc	ttc	cgc	480
Glu	Ser	Pro	Gly	Cys	Leu	Glu	Ala	Ser	Val	Thr	Phe	Asn	Leu	Phe	Arg	

145	150	155	160
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ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc	528		
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val			
165	170	175	

tga	531
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Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Lys Asp
35 40 45
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175